Claims

1. A method for assessing the prognosis of Ewing's Sarcoma (ES) patients comprising determining the expression pattern of a defined set of genes in tumor material obtained from said patients, and assigning said expression pattern to either a good prognosis or poor prognosis group.

2. The method according to claim 1, wherein the expression pattern of the aforementioned defined set of genes is determined by means of a technique selected from the group consisting of nucleic acid hybridization, semi-quantitative RT-PCR, quantitative real time RT-PCR, immunohistochemistry and ELISA.

3. The method according to claim 2, wherein the expression pattern of the aforementioned defined set of genes is determined by means of a nucleic acid hybridization technique.

4. The method according to claim 3, wherein the nucleic acid hybridization technique comprises the steps of extracting total RNA from the ES-patient tumor material, generating double-stranded cDNA from said total RNA, performing *in vitro* transcription of said cDNA, labeling the RNA transcript obtained thereby, hybridization of said RNA transcript to a solid-state human genome microarray.

5. The method according to claim 1, wherein the assignment of the gene expression pattern to one of the good or poor prognosis groups is performed by means of a hierarchical clustering technique.

6. The method according to claim 1, wherein the defined set of genes comprises genes selected from a group of 818 genes listed in Table 1, hereinabove.

7. The method according to claim 6, wherein the defined set of genes consists of between 1 and 100 genes selected from the group of 818 genes.

8. The method according to claim 6, wherein the defined set of genes consists of between 101 and 200 genes selected from the group of 818 genes.

9. The method according to claim 6, wherein the defined set of genes consists of between 201 and 300 genes selected from the group of 818 genes.

10. The method according to claim 6, wherein the defined set of genes consists of between 301 and 400 genes selected from the group of 818 genes.

11. The method according to claim 6, wherein the defined set of genes consists of between 401 and 500 genes selected from the group of 818 genes.

12. The method according to claim 6, wherein the defined set of genes consists of between 501 and 600 genes selected from the group of 818 genes.

13. The method according to claim 6, wherein the defined set of genes consists of between 601 and 700 genes selected from the group of 818 genes.

14. The method according to claim 6, wherein the defined set of genes consists of between 701 and 818 genes selected from the group of 818 genes.

15. A solid-state nucleic acid microarray comprising at least two nucleic acids affixed to a substrate, wherein each of said at least two nucleic acids consists of a partial sequence of one of the genes present in the group of 818 genes listed in Table 1, hereinabove.

16. The solid-state nucleic acid microarray according to claim 15 comprising 818 nucleic acid sequences, wherein each of said sequences consists of a partial sequence of one of the 818 genes listed in Table 1, hereinabove.

17. The solid-state nucleic acid microarray according to claim 15 further comprising one or more control nucleic acid sequences.

18. A kit comprising a solid-state nucleic acid microarray according to claim 15, together with an instruction sheet.